

us-09-052-089a-5.rspt

P 5 10:01:16 2002

Copyright (c) 1993 - 2000 Compugen Ltd.
GenCore version 4.5

OM protein - protein search, using SW model

Run on: September 4, 2002, 16:16:07 ; Search time 172.18 seconds
(without alignments)
{without alignments)
(without alignments)
updates/sec

Title: US-09-052-089A-5
Perfect score: 286

Scoring table: BL2SUM62

Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_19.*

1: sp_archae: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_invertebrate: *
5: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rhodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SPREMBL_19.*

ALIGNMENTS

RESULT	1	PRT;	469 AA.
ID 000467	PRELIMINARY;		
ID 000467;	000467; (Created)		
AC 000467;	000467; (REMBIrel. 04, Last sequence update)		
DT 01-JUL-1997	01-JUL-1997 (REMBIrel. 04, Last sequence update)		
DT 01-JUL-1997	01-JUL-1997 (REMBIrel. 19, Last annotation update)		
DT 01-DEC-2001			
DE HTRIP.			
OS Homo sapiens (Human).			
OS Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
OC NCBI-TaxID=9606;			
OX [1]			
RN SEQUENCE FROM N.A.			
RX MBDLINE:97258120; PubMed:9104814;			
DR Lee, S.Y.; Lee, S.Y.; Choi, Y.;			
DR Lee, S.Y.; Lee, S.Y.; Choi, Y.;			
RT "TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR)- and CD36-TRAF signaling complexes that inhibits TRAF2-mediated NF- κ B activation."			
RT J. Exp. Med. 185:1275-1285(1997).			
RL -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
CC DR EMBL; 077845; AAB52933; 1.			
CC DR InterPro; IPR001841; Znf_finger.			
CC DR Pfam; PF00097; ZF-C3HC4; 1.			
CC DR SMART; SM00184; RING; 1.			
CC DR Zinc-finger.			
CC KW SEQUENCE 469 AA; 53138 MN; 2D54ED04B84ABAE4 CRC64;			
CC SO			
Query Match 96.2%; Score 275; DB 4; Length 469;			
Best Local Similarity 96.1%; Pred. No. 1; 2e-29; 1; Indels 0; Gaps 0;			
Matches 49; Conservative 1; Mismatches 1; Gaps 0;			
QY 1 RALECTICSDFFDHSDRVAMDCGHTFHQCLQSFETAPSRTCPQCRIQVG 54			
Db 4 RALECTICSDFFDHSDRVAMDCGHTFHQCLQSFETAPSRTCPQCRIQVG 54			

RESULT 2 PRELIMINARY; PRT; 223 AA.
 ID 0922NB ID 0922NB PRELIMINARY; PRT; 223 AA.
 AC 0922NB; OC
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE TRAF-INTERACTING PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus musculus (Mouse).
 OC NCBI_TaxID=10090;
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=2108560; PUBMED=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Haru A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA aizawa K., Izawa M., Nishii K., Kurosawa H., Kondo S., Yamamoto T.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Niiyado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh R.,
 RA Blakely J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee M.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Winstaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT Functional annotation of a full-length mouse cDNA collection.;
 RL Nature 409:685-690 (2001).
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AR012948; BAB28567.1; -.
 DR MGII:1096377; TraIP.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW ZINC-finger.
 SQ SEQUENCE. 470 AA; 53149 MW; EBFABC49A9F4BF2E CRC64;

RESULT 3 PRELIMINARY; PRT; 469 AA.
 ID 09BWF2 ID 09BWF2 PRELIMINARY; PRT; 469 AA.
 AC 09BWF2; OC
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE TRAF-INTERACTING PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE-LUNG CARCINOMA;
 RA Strausberg R.;
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; BC000310; ARH0010.1; -.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW ZINC-finger.
 SQ SEQUENCE. 469 AA; 53294 MW; B9EF3B08FBC5985B CRC64;

RESULT 4 PRELIMINARY; PRT; 470 AA.
 ID 09CPP4 ID 09CPP4 PRELIMINARY; PRT; 470 AA.
 AC 09CPP4; OC
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TRAF-INTERACTING PROTEIN.
 GN TRAIP.

RESULT 5 PRELIMINARY; PRT; 470 AA.
 ID 008854 ID 008854 PRELIMINARY; PRT; 470 AA.
 AC 008854; OC
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MTRIP.
 RN [1]
 RP SEQUENCE FROM N. A.
 RA MEDLINE=9725620; PUBMED=9104814;
 RA Lee S.Y., Lee S.Y., Choi Y.;
 RA *TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR) and c-Jun-NTRAF signaling complexes that inhibits TRAF2-mediated NF-kappaB activation.;
 RL J. Exp. Med. 185:1275-1285 (1997).
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; 077844; ARB5294.1; -.
 DR MGII:1096377; traip.
 DR InterPro; IPR001841; Znf_fing.

DR P_fam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW zinc_finger.
 SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

Query Match 90.9%; Score 260; DB 11; Length 470;
 Best Local Similarity 92.0%; Pred. No. 1.4e-27; 2; Mismatches
 Matches 46; Conservative 2; Indels 0; Gaps 0;
 Kw 5 SLC7CSDFFDHSRDAVAAHCQHNFHQCLQIWFETAPSRTCPQCRIQVG 54

RESULT 6

Q9YGN2 PRELIMINARY; PRT; 433 AA.

AC Q9YGN2; -
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRAF interacting protein
 TRIP.
 GN Fugu rubripes (Japanese pufferfish) (Takifugu rubripes),
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 RA Elgar G., Cottage A.J., Clark M., Hawker K., Umrania Y., Wheller D., Bishop M.,
 RT "Three receptor genes for plasminogen related growth factors in the
 genome of the puffer fish Fugu rubripes.",
 RL PEBs Lett. 43:370-374(1999).
 CC -
 DR EMBL; AJ010317; CA090841; -
 DR InterPro; IPR01841; Znf_finger.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW zinc_finger.
 SEQUENCE FROM N.A.
 RX MEDLINE=9914883; PubMed=10025966;
 RA Cottage A.J., Clark M., Hawker K., Umrania Y., Wheller D., Bishop M.,
 RA Elgar G.,
 RT "Three receptor genes for plasminogen related growth factors in the
 genome of the puffer fish Fugu rubripes.",
 RL PEBs Lett. 43:370-374(1999).
 CC -
 DR EMBL; AJ010317; CA090841; -
 DR InterPro; IPR01841; Znf_finger.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 CC Submitted (MAR-2000) to the EMBL/GenBank/NCBI databases.
 DR -
 EMBL; AAC005496; AAC3521/1; -
 DR HSSP; P28990; ICHC.
 DR InterPro; IPR01841; Znf_finger.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW zinc-finger.
 SQ SEQUENCE 310 AA; 35390 MW; BEEC140152F5E2C CRC64;

Query Match 39.9%; Score 114; DB 10; Length 310;
 Best Local Similarity 39.6%; Pred. No. 1e-07; 11; Mismatches
 Matches 19; Conservative 11; Indels 16; Gaps 2; 1;
 Kw 3 LCTICSDFFDHSRDAVAAHCQHNFHQCLQIWFETAPSRTCPQCRIQVG 50

RESULT 8

Q9YGN6 PRELIMINARY; PRT; 420 AA.

AC Q9YGN6; -
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE R31343_1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreate P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
 RA Dangnan L., Eiler A., Christensen M., Georgescu A., Avilla J., Liu S.,
 RA Attix C., Andreise T., Tranthem M., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrasco A.V.;
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/NCBI databases.
 CC -
 DR EMBL; AAC00574; AAC62458; 1; -
 DR InterPro; IPR00561; EGF-like.
 DR InterPro; IPR003137; PA.
 DR InterPro; IPR001841; Znf_finger.
 DR Pfam; PF02225; PA; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 KW zinc-finger.
 SQ SEQUENCE 420 AA; 45880 MW; 572731A8EBA97FCE CRC64;

Query Match 39.9%; Score 114; DB 4; Length 420;
 RC STRAIN=CV. COLUMBIA;

Best Local Similarity	Pred. No.	Indels	Gaps
37.5%	1.4e-07;	0;	0;
Matches	18;	Conservative	9;
Mismatches	21;	Indels	0;
QY	3	LCTCISDFDFHSDYVAAMDCGHFPHLQLIQSETASRTCPQCRIQV 50	
Db	299	LCATCILDEVEGDQLKILPCSHTYHCKC1DPWWSQAPRRSCPVCKQS 346	
RESULT	9	PRELIMINARY;	PRT;
ID	Q95SS5		435 AA.
AC	Q95SS5;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	GH03577P.		
GN	CG5140.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN="CN BW SP";		
RA	Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J., Farfan D., Frise E., George R., Champé M., Chavez C., Dorsett V., Liao R., Liao P., Miranda A., Mongailo C.J., Gonzalez M., Guarin H., Li P., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., Nuno J., Pacleb J., Parqas V., Park S., Phouanenavong S., Wan K., Yun C., Lewis S.E., Robin G.M., Celinker S., Submitted (FOCT-2001) to the EMBL/GenBank/DBJ databases.		
RA	RH000001; EMBL:AY060610; ASN:8158; 1;		
DR	EMBL:AY060610; ASN:8158; 1;		
DR	SEQUENCE 435 AA; 48455 MW; 0BFF0AC81DD9416E CRC64; SQ		
RESULT	10		
Q9V8D7	09V8D7	PRELIMINARY;	PRT;
AC	09V8D7;		455 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
QY	4	CTICSDFFDHSDYVAAMDCGHFPHLQLIQSETASRTCPQC 47	
Db	6	CVICAEELFGQADEVFATVGHMFHNCLNQWLDL--SKTCQC 47	
RESULT	10		
Q9V8D7	09V8D7	PRELIMINARY;	PRT;
AC	09V8D7;		455 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	CG5140. PROTEIN.		
GN	Drosophila melanogaster (Fruit fly).		
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN="BERKELEY"; MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worfman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfleiffer B.D., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin E.M., Ballew R.M., Basu P.V., Baxendale J.P., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bork P., Bortola D., Bortz K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Harris N.L., Harvey D., Heiman T.J., Howland T.J., Wei M.-H., Ibeagwam C., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., Ketchum K.A., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Jallal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Lai Z., Kimmel B.E., Koira C.D., Kraft C., Kravitz S., Kulp D., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shuping C., Sridharan S., St. Onge J., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirska S., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Robin G.M., Venter J.C., RT "The genome sequence of Drosophila melanogaster.", RLS Science 287:2185-2195(2000).		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR	EMBL: AE003800; ARF57730; 1.		
DR	EMBL: FBan0034314; CG54540.		
DR	InterPro: IPR001841; Znf-finger.		
DR	Pfam: PF00097; zf-C3H4; 1.		
DR	SMART: SM00184; RING; 1.		
KW	Zinc-finger.		
SQ	SEQUENCE 455 AA; 50726 MW; BEA74F4CACE8FD5B CRC64;		
RESULT	11		
Q9X5A4	09X5A4	PRELIMINARY;	PRT;
ID	Q9X5A4		158 AA.
AC	09X5A4;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	EG:2285.12 PROTEIN.		
GN	EG:2285.12 OR CG4325.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
OX	NCBI_TAXID=7272;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN="BERKELEY"; MEDLINE=20196005; PubMed=10731132;		
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worfman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfleiffer B.D., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin E.M., Ballew R.M., Basu P.V., Baxendale J.P., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bork P., Bortola D., Bortz K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Harris N.L., Harvey D., Heiman T.J., Howland T.J., Wei M.-H., Ibeagwam C., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., Ketchum K.A., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Jallal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Lai Z., Kimmel B.E., Koira C.D., Kraft C., Kravitz S., Kulp D., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shuping C., Sridharan S., St. Onge J., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirska S., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Robin G.M., Venter J.C., RT "The genome sequence of Drosophila melanogaster.", RLS Science 287:2185-2195(2000).		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR	EMBL: AE003800; ARF57730; 1.		
DR	EMBL: FBan0034314; CG54540.		
DR	InterPro: IPR001841; Znf-finger.		
DR	Pfam: PF00097; zf-C3H4; 1.		
DR	SMART: SM00184; RING; 1.		
KW	Zinc-finger.		
SQ	SEQUENCE 455 AA; 50726 MW; BEA74F4CACE8FD5B CRC64;		

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mayes A.D., Dew I., Ditz S.M.,
 RA Dodson K., Doup L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Fosler C., Gabrieleian A.E., Garg N.S., Galbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
 RA Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Murphy L., Muzny D.M.,
 RA Mount S.M., Moy M., Murphy B., Morris J., Moshefi A.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spadling A.C., Statileton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter J., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassaman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "the genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Submitted (APR-1999) to the EMBL/genBank/DBJ databases.
 RA Murphy L., Harris D., Barrell B.;
 RT "Sequencing the distal X chromosome of *Drosophila melanogaster*.";
 RL Submitted (SEP-1998) to the EMBL/genBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RA Benos P.;
 RL Submitted (APR-1999) to the EMBL/genBank/DBJ databases.
 RA Murphy L., Harris D., Barrell B.;
 RT "Sequencing the distal X chromosome of *Drosophila melanogaster*.";
 DR EMBL; AL031765; CA041708; 1; -;
 DR EMBL; AL031765; CA041708; 1; -;
 DR FLYBASE; FBgn0025878; EG:22E5; 12.
 DR InterPro; IPR001841; znf_fing.
 DR Pfam; PF00097; zf-CCHC4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 158 AA; 17741 MW; 21c417B040642D73 CRC64;
 RN

RESULT 13
 ID Q5RB5
 ID Q5RB5
 AC PRELIMINARY;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LD46221P.
 GN CG30916.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriodea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

[1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Y; CN BW SP;
 RA Stapleton M., Brokstein P., Hong L., Abganyan A., Carlson J.,
 RA Champre M., Chavez C., Dorsett V., Farfan D., Fiske E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Munagali C.J.,
 RA Nuneo J., Paclob J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,
 RL Submitted (OCT-2001) to the EMBL/genBank/DBJ databases.
 DR EMBL; KY061504; AAL295952; -;
 SQ SEQUENCE 263 AA; 29515 MW; B98CECE994071BFF CRC64;

RESULT 12
 ID Q9NQB
 ID Q9NQB
 AC PRELIMINARY;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE F6A14.12. PROTEIN.
 GN F6A14.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Arabidopsis; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicoyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RESULT 14
 ID Q9N3D1
 ID Q9N3D1
 AC PRELIMINARY;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 33.4 kDa PROTEIN.
 GN Y54E1QB.R.3.
 OS Caenorhabditis elegans.

RESULT 14
 ID Q9N3D1
 ID Q9N3D1
 AC PRELIMINARY;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 33.4 kDa PROTEIN.
 GN Y54E1QB.R.3.

KW zinc-finger.
SQ SEQUENCE 524 AA; 58471 MW; CFFC6AB4E39BD6FF CRC64;
Query Match 34.6%; Score 99; DB 10; Length 524;
Best Local Similarity 36.4%; Pred. No. 2e-05; Mismatches 8; Indels 18; Gaps 2; Gaps 1;
Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;
RESULT 24
ID 097260 PRELIMINARY; PRT; 1181 AA.
AC 097260;
DT 01-MAY-1999 (TREMBrel. 10, Created)
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
DE HYPOTHETICAL 135.6 KDA PROTEIN.
GN PRO0610C; MAU3P5.8
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jageski K., Jassal B., Kytes S., McLean J., Moulle S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Shelton J., Squares R., Sulston J. E.,
RA Whitehead S., Woodward C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum ".
RL Nature 400:532-536(1999).
CC !-- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AL034556; CB38971.1; -.
DR HSSP; P00097; zf-C3HC4; 1.
DR InterPro; IPR01841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM0084; RING; 1.
KW hypothetical protein; Zinc-finger.
SQ SEQUENCE 1181 AA; 135638 MW; 288C44EA4FB8C2D4 CRC64;
Query Match 34.6%; Score 99; DB 5; Length 1181;
Best Local Similarity 34.0%; Pred. No. 4.7e-05; Mismatches 16; Conservative 12; Mismatches 17; Indels 2; Gaps 1;
Matches 16; Conservative 12; Mismatches 17; Indels 2; Gaps 1;
RESULT 25
ID Q9LNU8 PRELIMINARY; PRT; 325 AA.
AC Q9LNU8;
DT 01-OCT-2000 (TREMBrel. 15, Created)
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
DE GB/AF27103.1
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bower L., Caminucci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narumiya M.,
RA Nguyen M., Onderka C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF028290; AAL16122.1; -.
SQ SEQUENCE 368 AA; 41618 MW; 79A48BD079A008E CRC64;
Query Match 34.3%; Score 98; DB 10; Length 368;
Best Local Similarity 34.1%; Pred. No. 2e-05; Mismatches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;
RESULT 27
ID Q9LMW3 PRELIMINARY; PRT; 383 AA.
AC Q9LMW3;

Query Match	34.3%	Score 98;	DB 5;	Length 621;		
Best Local Similarity	38.8%	Pred No.	3.3e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
	:					
Db	279	ICICREDWNVHSK--KLPCHFTCLRSWFQR--QQTCTPCTRLNI	322			
RESULT	30					
Q95SP2		PRELIMINARY;		PRT;		
ID	095SP2				626 AA.	
AC	Q95SP2					
DT	01-DEC-2001	(TREMBUREL. 19, Created)				
DT	01-DEC-2001	(TREMBUREL. 19, Last sequence update)				
DE	GH1117P;					
GN	CG1937.					
OS	Drosophila melanogaster (Fruit fly).					
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
OX	Phydroneidea; Drosophilidae; Drosophila.					
RN	[1]					
RP	SEQUENCE FROM N_A.					
RC	SPRAINLY, CN BW SP;					
RA	Stapleton M., Brookstein P., Hong L., Agbayani A., Carlson J.,					
RA	Champe M., Chavez C., Dorsett V., Farran D., Frise E., George R.,					
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,					
RA	Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,					
RA	Yu C., Lewis S.E., Rubin G.M., Celinker S.;					
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AY060577; AAL20225; 1; -.					
DR	SEQUENCE 626 AA; 69272 MW; F881B88D51D724EC CRC64;					
RESULT	31					
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy	3	LCTTC-SDFDFDSRVAAMDCGHFPHLOCLIQSFTAPSRTPQCRCQV	50			
Db	288	ICICREDWNVHSK--KLPCHFTCLRSWFQR-QQTCTPCTRLNI	331			
Query Match	34.3%	Score 98;	DB 5;	Length 626;		
Best Local Similarity	38.8%	Pred. No.	3.4e-05;			
Matches	19;	Conservative	8;	Mismatches	16;	Indels
					6;	Gaps
					3;	
Qy</						

RESULT	33	PRELIMINARY;	PRT;	439 AA.
ID	Q94GW2			
AC	Q94GW2			
DT	01-DEC-2001 (TREMBREL. 19, Created)			
DT	01-MAY-2000 (TREMBREL. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)			
DE	PUTATIVE VIP2 PROTEIN.			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryzeae; Ehrhartoideae; Oryzeae; Oryza.			
OC	NCBI_TaxID=4530;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hsing Y.-T.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M., Lee P.-F., Su C.-L., Chen C.-S., Shaw J.-F.; "Oryza sativa PR0431G05 genomics sequence." Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: AC087551; AAK70903.1; -			
DR	SEQUENCE 439 AA; 47922 MW; A87073753260893 CRC64;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Best Local Similarity 38.3%; Pred. No. 3.8e-05; Matches 18; Conservative 4; Mismatches 22; Indels 3; Gaps 1;			
QY	4 CTICSDFF--DHSRDAAMDCGHTFLQCLQISFETAPSRTCPCCR 47			
Db	35 CSICLDAVVAAGGERSTARLQCGHFHLDCTIGSAFNAKGVMQCPNCR 81			
RESULT	34			
ID	Q9M4C5	PRELIMINARY;	PRT;	442 AA.
AC	Q9M4C5;			
DT	01-OCT-2000 (TREMBREL. 15, Created)			
DT	01-OCT-2000 (TREMBREL. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)			
DE	VIP2 PROTEIN.			
GN	Avena fatua.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Oryzeae; Avena.			
OC	NCBI_TaxID=499;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-20208057; PubMed-10743654;			
RT	"Identification and analysis of proteins that interact with the Avena fatua homologue of the maize transcription factor VIVIPAROUS 1.";			
RT	Plant J. 21:133-142 (2000) C1 - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
RL	EMBL: AJ251051; CAB75506.1; -			
DR	TRANSFAC; T05621; -			
DR	InterPro; IPR001841; Znf_ring.			
DR	Pfam; PF00097; zf-C3HC4; 1.			
DR	SMART; SM00184; RING; 1.			
DR	SMART; SM00449; SPRY; 1.			
DR	SMART; PS00018; ZINC_FINGER_C3HC4; 1.			
KW	Zinc-finger.			
FT	NON_TER			
SQ	SEQUENCE 504 AA; 57735 MW; E0B377F32A36D1B9 CRC64;			
RESULT	35			
ID	Q9UPQ4	PRELIMINARY;	PRT;	504 AA.
AC	Q9UPQ4;			
DT	01-MAY-2000 (TREMBREL. 13, Created)			
DT	01-MAY-2000 (TREMBREL. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)			
DE	KIAA1098 PROTEIN (FRAGMENT).			
GN	KIAA1098.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OC	NCBIM3; NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Tissue=Brain; MEDLINE-99397452; PubMed-10470851;			
RA	Kikuno R., Nagase T., Ishikawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.			
RT	"Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";			
RT	for large proteins in vitro.";			
RL	DNA Res. 6:197-205(1995).			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL: AB029031; BAA83050.1; -			
DR	InterPro; IPR01870; Gamma_carboxylse.			
DR	InterPro; IPR03877; SPRY.			
DR	InterPro; IPR00315; Znf_box.			
DR	InterPro; IPR01841; Znf_ring.			
DR	Pfam; PF00643; zf-B_box; 1.			
DR	Pfam; PF00097; zf-C3HC4; 1.			
DR	SMART; SM00336; BBOX; 1.			
DR	SMART; SM00184; RING; 1.			
DR	SMART; SM00449; SPRY; 1.			
DR	SMART; PS00018; ZINC_FINGER_C3HC4; 1.			
KW	Zinc-finger.			
FT	NON_TER			
SQ	SEQUENCE 504 AA; 57735 MW; E0B377F32A36D1B9 CRC64;			
RESULT	36			
ID	Q9M143	PRELIMINARY;	PRT;	506 AA.
AC	Q9M143;			
DT	01-OCT-2000 (TREMBREL. 15, Created)			
DT	01-OCT-2000 (TREMBREL. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)			
DE	PUTATIVE RING ZINC FINGER PROTEIN.			
GN	AT4G01270.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
OC	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Laijier B., Stoenkeling T., Stumpf J., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			

CC	- ! - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL: ALI61491; CAR80936; 1; -.
DR	InterPro: IPR001841; Znf_ring.
DR	Pfam: PF00097; zf-C3HC4; 1.
DR	SMART: SM00184; RING; 1.
KW	Zinc-finger.
SQ	SEQUENCE 506 AA; 56518 MW; 1B06751A4E299FE8 CRC64;
Query Match	33.4%; Score 95.5; DB 10; Length 506;
Best Local Similarity	39.6%; Pred. No. 6e-05;
Matches	21; Conservative 9; Mismatches 14; Indels 9; Gaps 3;
QY	2 ALCTICSD---FFFDISRDVAAMDCCGHTFHQLCQIQLQSFETAPS--RVCPOCR 47
ID	Q9ZVUB
AC	Q9ZVUB; PRELIMINARY;
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBLrel. 19, Last annotation update)
DE	T5A14_7. PROTEIN (ATIG55530/T5A14_7).
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Feederstiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altfati H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremener'skaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Wsotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W., Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Cheuk H., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Ishida J., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Kawai J., Lam B., Lee J.M., Jones T., Kamiya A., Karlin-Neumann G., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Soutthwick A., Tang C.C., Toriumi M., Yamada K., Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Banh J., Cheuk H., Carninci P., Kim C.J., Koesema E., Meyers M.C., Goldsmith A.D., Hayashizaki Y., Ishida J., Carninci P., Dale J.M., Gibson H.A., Kamiya A., Karlin-Neumann G., Kawai J., Lee J.M., Jones T., Lam B., Li S.X., Miranda G., Miranda J., Niguen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Soutthwick A., Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN	- ! - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL: AC005223; AADD0644; 1; -.
DR	EMBL: AF424578; AALL1572; 1; -.
DR	EMBL: AY039608; AAK62662; 1; -.
DR	InterPro: IPR001841; Znf_ring.
DR	Pfam: PF00097; zf-C3HC4; 1.
DR	SMART: SM00184; RING; 1.
KW	Zinc-finger.
SQ	SEQUENCE 351 AA; 38963 MW; DE5ABB4D72CF7075 CRC64;
Query Match	33.2%; Score 95; DB 10; Length 351;
Best Local Similarity	38.3%; Pred. No. 4.8e-05;
Matches	18; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
QY	4 CTICSDFFDHSDVAAMDCCGHTFHQLCQIQLQSFETAPSRTPOCRIV 50
ID	Q9NSR1
AC	Q9NSR1; PRELIMINARY;
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 15.7 kDa PROTEIN (LIKELY ORTHOLOG OF MOUSE ARKADIA).
GN	DKFZP761D081.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606; [1]
RP	SEQUENCE FROM N.A.
RC	TISSUE: AMYGDALA;
RA	Ortenwaldner B., Obermaier B., Mewes H.W., Weil B., Wiemann S., Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE-BRAIN; PRIMITIVE NEUROECTODERMAL;
RA	Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL	DR EMBL; ALI57474; CAN75699; 1; -.
RA	DR BC010369; AAI01369; 1; -.
RA	DR InterPro: IPR001841; Znf_ring.
DR	Pfam: PF00097; zf-C3HC4; 1.
DR	SMART: SM00184; RING; 1.
KW	Hypothetical protein; Zinc-finger.
SQ	SEQUENCE 137 AA; 15739 MW; 6AA62DC6CEE8C114 CRC64;
Query Match	32.9%; Score 94; DB 4; Length 137;
Best Local Similarity	36.2%; Pred. No. 2.5e-05;
Matches	17; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY	4 CTICSDFFDHSDVAAMDCCGHTFHQLCQIQLQSFETAPSRTPOCRIV 50
ID	Q942E6
AC	Q942E6; PRELIMINARY;
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	PUTATIVE PGD14 PROTEIN (POLEN GERMINATION RELATED PROTEIN).
GN	PO480C01; 20.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioidae; Oryzeae; Oryza.
OC	NCBI_TaxID=4530; [1]
RP	SEQUENCE FROM N.A.
RC	SEQUIN=CV; NIPPONBARE;
RA	Sasaki T., Matsumoto T., Yamamoto K.;
RT	"Oryza sativa, nipponbare (GA3) genomic DNA."

Thu Sep 5 10:01:16 2002

RL Submitted (MAR-2001) to the EMBL/GenBank/NCBI databases.
 DR EMBL: APO03453; BAB68060; -;
 SEQUENCE 299 AA; 34096 MW;
 SQ 62A8588E4PACC517 CRC64;

Query Match 32.9%; Score 94; DB 10; Length 299;
 Best Local Similarity 38.6%; Pred. No. 5.6e-05;
 Matches 17; Conservative 9; Mismatches 16; Indels 2; Gaps 2;
 QY 4 CTICSDDF-EDRSRDAAMDCGHTFHQCLQSETASRSTCQC 46
 DB 194 CPICFEYLFFESTNDVSVLPCGHTHVKCL-REMEHCOFACPLC 236

RESULT 40

Q90ZT8 PRELIMINARY; PRT; 879 AA.

ID Q90ZT8;
 AC Q90ZT8;
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RING FINGER PROTEIN (FRAGMENT).
 GN ARKADIA.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TAXID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=11298452;
 RX MEDLINE=21195911;
 RA Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L.,
 RA Swan D.;
 RT "Induction of the mammalian node requires Arkadia function in the
 extraembryonic lineages";
 RT Nature 410:825-830(2001).
 RL EMBL: AF329846; AAK38636; 1; -.
 FT NON_TER 1
 SEQUENCE 879 AA; 95701 MW; EC8564B228053264 CRC64;

Query Match 32.9%; Score 94; DB 13; Length 879;
 Best Local Similarity 36.2%; Pred. No. 0.00017;
 Matches 17; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
 QY 4 CTICSDDFDHSRDAAMDCGHTFHQCLQSETASRSTCQC 50
 DB 827 CTICSDDFDHSRDAAMDCGHTFHQCLQSETASRSTCQC 871

Search completed: September 4, 2002, 16:16:08
 Job time: 1492 sec